

SEE WD NO. 1

Database : UniProt\_02:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1328	99.6	<u>349</u>	1	GUB_FIBSU	P17989 fibrobacter
2	266.5	20.0	259	1	GUB_BACBR	P37073 bacillus br
3	266.5	20.0	851	2	Q9K7X5	Q9k7x5 bacillus ha
4	248.5	18.6	256	2	Q9APD8	Q9apd8 bacillus ci
5	247.5	18.6	276	2	Q45648	Q45648 bacillus sp
6	245.5	18.4	214	2	Q8GMY0	Q8gmy0 bacillus li
7	245.5	18.4	242	1	GUB_BACSU	P04957 bacillus su
8	244.5	18.3	215	2	Q84GK1	Q84gk1 bacillus li
9	243	18.2	334	2	Q84C00	Q84c00 clostridium
10	242.5	18.2	214	2	Q93GE8	Q93ge8 uncultured
11	242.5	18.2	802	1	XYND_RUMFL	Q53317 ruminococcu
12	242.5	18.2	802	2	Q9S310	Q9s310 ruminococcu
13	241.5	18.1	214	2	Q93GE7	Q93ge7 uncultured

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

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# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1328	99.6	349	2	A44507	licheninase (EC 3.
2	266.5	20.0	851	2	H84053	endo-beta-1,3-1,4
3	265.5	19.9	252	2	A48378	licheninase (EC 3.
4	247.5	18.6	276	2	I40453	licheninase (EC 3.
5	245.5	18.4	242	1	LXBS	licheninase (EC 3.
6	242.5	18.2	802	2	A36910	xylanase, beta(1,3
7	238.5	17.9	239	1	A29091	licheninase (EC 3.
8	237	17.8	334	1	S23498	licheninase (EC 3.
9	229.5	17.2	243	1	S15388	licheninase (EC 3.
10	226	17.0	237	1	S11927	licheninase (EC 3.
11	225	16.9	238	1	S19012	licheninase (EC 3.

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1103	82.7	228	3	US-09-286-690-12	Sequence 12, Appl
2	257.5	19.3	308	4	US-09-463-862A-1	Sequence 1, Appli
3	245.5	18.4	242	3	US-09-286-690-8	Sequence 8, Appli
4	244	18.3	239	1	US-08-103-998-2	Sequence 2, Appli
5	231.5	17.4	279	3	US-09-286-690-9	Sequence 9, Appli
6	229.5	17.2	243	3	US-09-286-690-10	Sequence 10, Appl
7	225	16.9	238	3	US-09-286-690-7	Sequence 7, Appli
8	222.5	16.7	242	3	US-09-286-690-11	Sequence 11, Appl
9	220.5	16.5	237	1	US-08-103-998-4	Sequence 4, Appli
10	200.5	15.0	526	4	US-09-248-796A-14807	Sequence 14807, A
11	189	14.2	245	3	US-09-286-690-2	Sequence 2, Appli
12	185	13.9	462	4	US-09-248-796A-14808	Sequence 14808, A

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query					Description
	Score	Match	Length	DB	ID	
1	257.5	19.3	308	2	AAW93001	Aaw93001 B. alkalo
2	246.5	18.5	242	1	AAP95000	Aap95000 Bacillus
3	244	18.3	214	4	AAE07317	Aae07317 Barley re
4	244	18.3	239	2	AAR06621	Aar06621 Hybrid (1
5	230	17.3	212	5	ABP58995	Abp58995 Paenibaci
6	226	17.0	234	2	AAR03775	Aar03775 Thermosta
7	226	17.0	237	2	AAR05803	Aar05803 Heat-stab
8	225	16.9	208	5	ABB76858	Abb76858 Bacterial
9	225	16.9	214	5	ABB76859	Abb76859 Bacterial
10	220.5	16.5	237	2	AAR06622	Aar06622 Hybrid (1
11	204.5	15.3	504	8	ADP98858	Adp98858 C. albica
12	189	14.2	245	2	AAW37884	Aaw37884 Lichenase
13	185	13.9	453	7	ADC01836	Adc01836 C. albica
14	185	13.9	453	8	ADP98992	Adp98992 C. albica

See 19 NO. 2

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
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 4: pir4:\*

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# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2020.5	70.5	720	2	T52564	Mre11 protein homo
2	852.5	29.8	649	1	S58097	probable dna repai
3	768	26.8	692	1	S57592	probable phosphoes
4	724	25.3	772	2	T27512	hypothetical prote
5	178	6.2	443	1	G69378	probable phosphoes
6	175.5	6.1	423	2	E75103	phosphoesterase ho
7	174.5	6.1	413	1	D71083	probable phosphoes
8	163.5	5.7	587	1	E69171	phosphoesterase-re
9	150.5	5.3	381	2	C90395	DNA repair protein
10	143	5.0	1038	2	JC5497	claustrin - chicke
11	141.5	4.9	409	2	E72765	probable phosphoes
12	136	4.7	1957	2	T38077	hypothetical coile

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

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#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2864	100.0	552	4	US-09-835-654-2	Sequence 2, Appli
2	2020.5	70.5	720	3	US-09-480-921B-8	Sequence 8, Appli
3	954.5	33.3	680	4	US-09-538-092-1165	Sequence 1165, Ap
4	768	26.8	692	4	US-09-538-092-632	Sequence 632, App
5	507.5	17.7	270	4	US-09-248-796A-19151	Sequence 19151, A
6	141.5	4.9	132	4	US-09-270-767-33195	Sequence 33195, A
7	141.5	4.9	132	4	US-09-270-767-48412	Sequence 48412, A
8	136	4.7	857	4	US-09-248-796A-20522	Sequence 20522, A
9	122	4.3	1120	3	US-09-147-404-1	Sequence 1, Appli
10	122	4.3	1935	4	US-09-538-092-916	Sequence 916, App